

Comprehensive characterization of the transcriptional landscape in Alzheimer's disease (AD) brains

Chengxuan Chen^{1,2,3*}, Zhao Zhang^{4,*}, Yuan Liu^{1,2,3,*}, Wei Hong^{4,*}, Hande Karahan^{5,6}, Jun Wang^{7,8}, Wenbo Li^{4,8}, Lixia Diao⁹, Meichen Yu^{10,11,12}, Andrew J. Saykin^{10,11,12}, Kwangsik Nho^{10,11,13}, Jungsu Kim^{5,6}, Leng Han^{1,2,3,10,13,#}. *These authors contributed equally.

¹Department of Biostatistics and Health Data Science, School of Medicine, Indiana University, Indianapolis, IN 46202, USA, ²Brown Center for Immunotherapy, School of Medicine, Indiana University, Indianapolis, IN 46202, USA, ³Center for Epigenetics and Disease Prevention, Institute of Biosciences and Technology, Texas A&M University, Houston, TX 77030, USA, ⁴Department of Biochemistry and Molecular Biology, The University of Texas Health Science Center at Houston McGovern Medical School, Houston, TX 77030, USA, ⁵Stark Neurosciences Research Institute, Indiana University School of Medicine, Indianapolis, IN 46202, USA, ⁶Department of Medical and Molecular Genetics, Indiana University School of Medicine, Indianapolis, IN 46202, USA, ⁷Department of Pediatrics, McGovern Medical School at The University of Texas Health Science Center at Houston, Houston, TX 77030, USA, ⁸Graduate School of Biomedical Sciences, The University of Texas MD Anderson Cancer Center and UTHealth, Houston, 77030, TX, USA, ⁹Department of Bioinformatics and Computational Biology, The University of Texas MD Anderson Cancer Center, Houston, TX 77030, USA, ¹⁰Indiana Alzheimer's Disease Research Center, Indiana University School of Medicine, Indianapolis, IN 46202, USA, ¹¹Department of Radiology and Imaging Sciences, Indiana University School of Medicine, Indianapolis, IN 46202, USA, ¹²Indiana University Network Science Institute, Bloomington, IN, USA, ¹³Center for Computational Biology and Bioinformatics, Indiana University School of Medicine, Indianapolis, IN 46202, USA.

Alzheimer's disease (AD) is the most common dementia among the elderly with multiple underlying etiology. Although how protein-coding genes affect the onset and progression of AD has been investigated extensively, the role of non-coding RNAs (ncRNAs) and post-transcription regulation (PTM) events in AD pathogenesis remains largely unknown. Here we used 1,234 AD RNA-seq data across six brain regions from the Mount Sinai/JJ Peters VA Medical Center Brain Bank Study (MSBB) and Mayo cohorts with multiple AD traits. We comprehensively characterized the landscape of ncRNAs, such as 33,321 long ncRNAs (lncRNAs) and 106,990 enhancer RNAs (eRNAs), and PTM events including 127,403 alternative polyadenylation (APA) events and 900,207 A-to-I RNA editing events. We also identified 32,220 aberrantly expressed ncRNAs and altered PTM events along with AD traits. To explore the potential roles of ncRNAs and PTM events in AD, we identified 236,932 significant associations between ncRNAs/PTM events and protein-coding genes to build regulatory networks. Furthermore, we developed a user-friendly data portal, AD Atlas (https://hanlaboratory.com/AD_atlas/), to facilitate users to browse, search, query, and download ncRNA and PTM events and their relevance in AD brains. Our study aims to establish a comprehensive data platform of ncRNAs and PTMs in AD, offering a valuable resource for the broader research community in the study of AD.

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